

Amendments to the Specification

Please replace the paragraph beginning at line 9 on page 5 with the following amended paragraph:

Using the method of Benight et al. a family of 100 sequences was obtained using a computer algorithm to have optimal hybridization properties for use in nucleic acid detection assays. The sequence set of 100 oligonucleotides was characterized in hybridization assays, demonstrating the ability of family members to correctly hybridize to their complementary sequences with an absence of cross hybridization. These are the sequences having SEQ ID NOs: ~~1 to 100~~ 1173 to 1272 of Table I. This set of sequences has been expanded to include an additional 110 sequences that can be grouped with the original 100 sequences as having non-cross hybridizing properties, based on the characteristics of the original set of 100 sequences. These additional sequences are identified as SEQ ID NOs: ~~101 to 210~~ 1273 to 1382 of the sequences in Table I. How these sequences were obtained is described below.

Please replace the paragraph beginning at line 10 on page 12 with the following amended paragraph:

A phantom sequence may thus be generated from exemplary Sequence 1 and Sequence 2 as follows:

Sequence 1: ATGTTTAGTGAAAAGTTAGTATTG (SEQ ID NO:1383)

 * •

Sequence 2: ATGTTAGTGAATAGTATAGTATTG (SEQ ID NO:1384)

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Phantom Sequence: ATGTTAGTGAAAGTTAGTATTG

Please replace the paragraph beginning at line 32 on page 53 with the following amended paragraph:

A preferred family of 100 tags is shown as SEQ ID NOs: ~~1 to 100~~ 1173 to 1272 in Table I. Characterization of the family of 100 sequence tags was performed to determine the ability of these sequences to form specific duplex structures with their complementary sequences and to assess the potential for cross hybridization. The 100 sequences were synthesized and spotted onto glass slides where they were coupled to the surface by amine linkage. Complementary tag sequences were Cy3-labeled and hybridized individually to the array containing the family of 100 sequence tags. Formation of duplex structures was detected and quantified for each of the positions on the array. Each of the tag sequences performed as expected, that is the perfect match duplex was formed in the absence of significant cross hybridization under stringent hybridization conditions. The results of a sample hybridization are shown in Figure 1. Figure 1a shows the hybridization pattern seen when a microarray containing all 100 probes was hybridized with the target complementary to probe 181234. The 4 sets of paired spots correspond to the probe complementary to the target. Figure 1b shows the pattern seen when a similar array was hybridized with a mix of all 100 targets. These results indicate that the family of sequences which is the subject of this patent can be used as a family of non-cross hybridizing (tag) sequences.

Please replace the paragraph beginning at line 16 on page 54 with the following amended paragraph:

The family of 100 non-cross-hybridizing sequences can be expanded by incorporating additional tetramer sequences that are used in constructing further 24mer oligonucleotides. In one example, four additional words were included in the generation of new sequences to be considered for inclusion as non-cross talkers in a family of sequences that were obtained from the above method using 10 tetramers. In this case, the four additional words were selected to avoid potential homologies with all potential combinations of other words: YYXW (TTAG); WYYX (GTTA); YXXW (ATAG) and WYYY (GTTT). The total number of sequences containing six words using the 14 possible words is 14^6 or 7,529,536. These sequences were screened to eliminate sequences that contain repetitive regions that present potential hybridization problems such as four or more of a similar base (e.g., AAAA or TTTT) or pairs of G's. Each of these sequences was compared to the sequence set of the original family of 100 non-cross-hybridizing sequences (SEQ ID NOs: ~~1 to 100~~ 1173 to 1272). Any new sequence that contained a minimal threshold of homology (that does not include the use of insertions or deletions) such as 15 or more matches with any of the original family of sequences was eliminated. In other words, if it was possible to align a new sequence with one or more of the original 100 sequences so as to obtain a maximum simple homology of 15/24 or more, the new sequence was dropped. Simple homology" between a pair of sequences is defined here as the number of pairs of nucleotides that are matching (are the same as each other) in a comparison of two aligned sequences divided by the total number of potential matches. "Maximum simple homology" is obtained when two sequences are aligned with each other so as to have the maximum number of paired matching nucleotides. In any event, the set of new sequences so obtained was referred to as the "candidate sequences". One of the candidate sequences was arbitrarily chosen and referred to as sequence 101. All the candidate sequences were checked against sequence 101, and sequences that contained 15 or more non-consecutive matches (i.e., a maximum simple homology of 15/24 (62.5%) or more were

eliminated. This results in a smaller set of candidate sequences from which another sequence is selected that is now referred to as sequence 102. The smaller set of candidate sequences is now compared to sequence 102 eliminating sequences that contained 15 or more non-consecutive matches and the process is repeated until there are no candidate sequences remaining. Also, any sequence selected from the candidate sequences is eliminated if it has 13 or more consecutive matches with any other previously selected candidate sequence.

Please replace the paragraph beginning at lines 15 and 23 on page 55 with the following amended paragraphs, respectively:

The additional set of 73 tag sequences so obtained (SEQ ID NOS:~~101 to 173~~ 1273 to 1345 of Table 1) is composed of sequences that when compared to any of SEQ ID NOS:~~1 to 100~~ 1173 to 1272 of Table I have no greater similarity than the sequences of the original 100 sequence tags of Table I. The sequence set as derived from the original family of non cross hybridizing sequences, SEQ ID NOS:~~1 to 173~~ 1173 to 1345 of Table 1, are expected to behave with similar hybridization properties to the sequences having SEQ ID NOS:~~1 to 100~~ 1173 to 1272 since it is understood that sequence similarity correlates directly with cross hybridization (Southern et al., Nat. Genet.; 21, 5-9: 1999).

The set of 173 24mer oligonucleotides were expanded to include those having SEQ ID NOS:~~174 to 210~~ 1346 to 1382 as follows. The 4mers WXYW, XYXW, WXXW, WYYW, XYYX, YXYX, YXXY and XYXY where W=G, X=A, and Y=U/T were used in combination with the fourteen 4mers used in the generation of SEQ ID NOS:~~1 to 173~~ 1173 to 1345 to generate potential 24-base oligonucleotides. Excluded from the set were those containing the sequence patterns GG, AAAA and TTTT. To be included in the set of additional 24mers, a sequence also had to have at least one of the 4mers containing two G's: WXYW (GATG), WYXW (GTAG), WXXW (GAAG), WYYW (GTTG) while also containing exactly six G's. Also

required for a 24mer to be included was that there be at most six bases between every neighboring pair of G's. Another way of putting this is that there are at most six non-G's between any two G's. Also, each G nearest the 5'-end of its oligonucleotide (the left-hand side as written in Table I) was required to occupy one of the first to seventh positions (counting the 5'- terminal position as the first position.) A set of candidate sequences was obtained by eliminating any new sequence that was found to have a maximum simple homology of 16/24 or more with any of the previous set of 173 oligonucleotides (Table 1, SEQ ID NOs:~~1 to 173~~ 1173 to 1345). As above, an arbitrary 174th sequence was chosen and candidate sequences eliminated by comparison therewith. In this case the permitted maximum degree of simple homology was 16/24. A second sequence was also eliminated if there were ten consecutive matches between the two (i.e., it was notionally possible to generate a phantom sequence containing a sequence of 10 bases that is identical to a sequence in each of the sequences being compared). A second sequence was also eliminated if it was possible to generate a phantom sequence 20 bases in length or greater.

Please replace the paragraphs beginning at lines 1 and 4 on page 57 with the following amended paragraphs, respectively:

The selection of sequences using this approach would be amenable to a computerized process. Thus for example, a string of 10 contiguous bases of the first 24mer of Table I could be selected: GATTGTATTGATTGAGATTAAAG (SEQ ID NO:1173).

A string of contiguous bases from the second 24mer could then be selected and compared for maximum homology against the first chosen sequence: TGATTGTAGTATGTATTGATAAAG (SEQ ID NO:1174).

Please replace the paragraph beginning at line 1 on page 64 with the following amended paragraph:

A practical example of the aforementioned description is as follows:
For exon 1 of the human p53 tumor suppressor gene sequence the
following tag-Reverse primer (SEQ ID NO:1171) was generated:

222087

222063

5'-PO4-GATTGTAAGATTTGATAAAGTGTA-TCCAGGGAAGCGTGTCACCGTCGT-3'

Tag Sequence # 3

Exon 1 Reverse

The numbering above the Exon-1 reverse primer represents the genomic
nucleotide positions of the indicated bases.

The corresponding Exon-1 Forward primer sequence (SEQ ID NO:1172) is
as follows:

221873

221896

5'-Biotin-TCATGGCGACTGTCCAGCTTTGTG-3'

Please replace Table 1 beginning on page 87 with the following amended Table 1.

| | SEQ ID NO (1) | Sequence | No Assigned in Example 3 |
|----|---------------|--------------------------|--------------------------|
| 1 | <u>1173</u> | GATTTGTATTGATTGAGATTAAAG | 1 |
| 2 | <u>1174</u> | TGATTGTAGTATGTATTGATAAAG | 2 |
| 3 | <u>1175</u> | GATTGTAAGATTTGATAAAGTGTA | 3 |
| 4 | <u>1176</u> | GATTTGAAGATTATTGGTAATGTA | 4 |
| 5 | <u>1177</u> | GATTGATTATTGTGATTTGAATTG | 5 |
| 6 | <u>1178</u> | GATTTGATTGTAAAAGATTGTTGA | 6 |
| 7 | <u>1179</u> | ATTGGTAAATTGGTAAATGAATTG | 7 |
| 8 | <u>1180</u> | ATTGGATTTGATAAAGGTAAATGA | |
| 9 | <u>1181</u> | GTAAGTAATGAATGTAAAAGGATT | 8 |
| 10 | <u>1182</u> | GATTGATTGATTGATTGATTGAT | |
| 11 | <u>1183</u> | TGATGATTAAAGAAAGTGATTGAT | |
| 12 | <u>1184</u> | AAAGGATTTGATTGATAAAGTGAT | |
| 13 | <u>1185</u> | TGTAGATTTGTATGTATGTATGAT | 10 |
| 14 | <u>1186</u> | GATTTGATAAAGAAAGGATTGATT | |
| 15 | <u>1187</u> | GATTAAAGTGATTGATGATTGTA | 11 |
| 16 | <u>1188</u> | AAAGAAAGAAAGAAAGAAAGTGTA | 12 |
| 17 | <u>1189</u> | TGTAAAAGGATTGATTGATGTA | |
| 18 | <u>1190</u> | AAAGTGTAGATTGATTAAAGAAAG | |
| 19 | <u>1191</u> | AAAGTTGATTGATTGAAAAGGTAT | |
| 20 | <u>1192</u> | TTGATTGAGATTGATTTTGAGTAT | |
| 21 | <u>1193</u> | TGAATTGATGAATGAATGAAGTAT | 15 |
| 22 | <u>1194</u> | GTAATGAAGTATGTATGTAAGTAA | |

| SEQ ID NO (1) | Sequence | No Assigned in Example 3 |
|---------------|--------------------------------|--------------------------|
| 23 | 1195 TGATGATTTGAATGAAGATTGATT | 16 |
| 24 | 1196 TGATAAAGTGATAAAGGATTAAAG | 17 |
| 25 | 1197 TGATTTGAGTATTTGAGATTTTGA | 18 |
| 26 | 1198 TGTAGTAAGATTGATTAAAGGTAA | |
| 27 | 1199 GTATAAAGGATTGATTTTGAAAAG | |
| 28 | 1200 GTATTTGAGTAAGTAATTGATTGA | 19 |
| 29 | 1201 GTAAAAAGTTGAGTATTGAAAAAG | |
| 30 | 1202 GATTTGATAAAGGATTTGTATTGA | |
| 31 | 1203 GATTGTATTGAAGTATTGTAAAAG | 20 |
| 32 | 1204 TGATGATTTTGATGAAAAAGTTGA | |
| 33 | 1205 TGATTTGAGATTAAAGAAAGGATT | 21 |
| 34 | 1206 TGATTGAATTGAGTAAAAAGGATT | 22 |
| 35 | 1207 AAAGTGTAAGGATTTGATGTAT | |
| 36 | 1208 AAAGGTATTTGAGATTTGATTGAA | |
| 37 | 1209 AAAGTTGAGATTTGAATGATTGAA | 23 |
| 38 | 1210 TGTATTGAAAAGGTATGATTTGAA | |
| 39 | 1211 GTATTGTATTGAAAAGGTAATTGA | 24 |
| 40 | 1212 TTGAGTAATGATAAAGTGAAGATT | |
| 41 | 1213 TGAAGATTTGAAGTAATTGAAAAG | 25 |
| 42 | 1214 TGAAAAAGTGTAGATTTTGAGTAA | 26 |
| 43 | 1215 TGTATGAATGAAGATTTGATTGTA | |
| 44 | 1216 AAAGTTGAGTATTGATTTGAAAAG | 27 |
| 45 | 1217 GATTTGTAGATTTGTATTGAGATT | |
| 46 | 1218 AAAGAAAGGATTTGTAGTAAGATT | 29 |
| 47 | 1219 GTAAAAAGAAAGGTATAAAGGTAA | 30 |
| 48 | 1220 GATTAAAGTTGATTGAAAAGTGAA | 31 |
| 49 | 1221 TGAAAAAGGTAATTGATGTATGAA | |
| 50 | 1222 AAAGGATTAAAGTGAAGTAATTGA | 33 |
| 51 | 1223 ATGAATTGGTATGTATATGAATGA | 34 |
| 52 | 1224 TGAAATGAATGAATGATGAAATTG | 35 |
| 53 | 1225 ATTGATTGTGAATGAAATGAATTG | 36 |
| 54 | 1226 ATTGAAAGATGAAAAGATGAAAAG | 37 |
| 55 | 1227 ATTGTTGAAAAGTGTAATGATTGA | 38 |
| 56 | 1228 ATGATGTAATGAAAAGATTGTGTGA | 39 |
| 57 | 1229 AAAGATTGAAAGATGATGTAATTG | |
| 58 | 1230 ATTGATGAGTATATTGTGTAGTAA | 41 |
| 59 | 1231 AAAGATTGTGTAATTGATGATGAA | |
| 60 | 1232 AAAGGTATATTGTGTAATGAGTAA | |
| 61 | 1233 TGTAATGAGTATTGTAATTGAAAG | 43 |
| 62 | 1234 GTATAAAGAAAGATTGGTAAATGA | 44 |
| 63 | 1235 TTGAGTAATTGAATTGTGAAATGA | 45 |
| 64 | 1236 TGTATTGAATGAATTGTTGATGTA | 46 |
| 65 | 1237 TGTAATTGGTAAATGAGTAAAAAG | |
| 66 | 1238 TGAATGAAATTGATGAGTATAAAAG | |
| 67 | 1239 GTAAGTAAATTGAAAAGATTGATGA | 49 |
| 68 | 1240 GTAAATGATGATATTGGTATATTG | 50 |
| 69 | 1241 ATTGTTGATGATTGATTGAAATGA | 51 |
| 70 | 1242 ATTGTGAAGTATAAAGATGATTGA | 52 |
| 71 | 1243 ATGAAAAGTTGAGTAAATTGTGAT | |
| 72 | 1244 ATGAATTGAAAAGTATTGAAAAAG | 54 |
| 73 | 1245 GTAAATTGATGAAAAGTTGATGAT | |
| 74 | 1246 AAAGTGATGTATATGAGTAAATTG | 56 |
| 75 | 1247 GTAATGATAAAGATGATGATATTG | 57 |

| SEQ ID NO (1) | Sequence | No Assigned in Example 3 |
|---------------|----------|---------------------------|
| 76 | 1248 | TTGAAAAGATTGGTAATGATATGA |
| 77 | 1249 | AAAGTGAAAAAGATTGATTGATGA |
| 78 | 1250 | ATTGATGAGATTGATTATTGTGTA |
| 79 | 1251 | ATGAGATTATTGGATTTGTAGATT |
| 80 | 1252 | TGAAGATTATGAATTGGTAAGATT |
| 81 | 1253 | ATTGGATTATGAGATTATGATTGA |
| 82 | 1254 | ATTGTTGAATTGGATTAAAGATGA |
| 83 | 1255 | AAAGATGAGTAAGTAAATTGGATT |
| 84 | 1256 | AAAGGTAAGATTATTGATGAAAAG |
| 85 | 1257 | ATTGATGAGATTAAAGTTGAATTG |
| 86 | 1258 | GATTATTGGATTATGAAAAGGATT |
| 87 | 1259 | GATTTGTAATTGTTGAGTAAATGA |
| 88 | 1260 | AAAGAAAGATTGTTGAGATTATGA |
| 89 | 1261 | GTATAAAGGATTTTGAATTGATGA |
| 90 | 1262 | TTGAGATTGTAAATGAATTGTTGA |
| 91 | 1263 | GTATATTGATTGTGTAATGAAAAG |
| 92 | 1264 | TGATATGAATTGGATTATTGGTAT |
| 93 | 1265 | ATGAATGATGAATGATGATTATTG |
| 94 | 1266 | ATGAATTGATTGGATTGTAATGAT |
| 95 | 1267 | GATTGTAATTGAGTAAATTGATGA |
| 96 | 1268 | GATTATTGGATTAAAGGTAAATGA |
| 97 | 1269 | ATTGTTGAATTGATGAGATTTGAT |
| 98 | 1270 | GATTATGAGTAAATTGATTGTGAT |
| 99 | 1271 | GATTATTGTTGATGAATGATATTG |
| 100 | 1272 | TGTAAAAGATTGAAAGGTATGATT |
| 101 | 1273 | GTATTTAGATGAGTTTGTAGATT |
| 102 | 1274 | TGAAGTTATGTAATAGAAAAGTGAT |
| 103 | 1275 | GTATGTATTGTATGTAGTTAATTG |
| 104 | 1276 | TGATATAGATAGTTAGATAGATAG |
| 105 | 1277 | ATGATGATGTATTGTAGTTATGAA |
| 106 | 1278 | TTAGTGAATGTATTAGTTGATGTA |
| 107 | 1279 | GTTAGTTAGATTATTGTTAGTTAG |
| 108 | 1280 | GTTAATTGTGTAGTTTGTATTATGA |
| 109 | 1281 | GTTATGAAATAGTGATATTGTTAG |
| 110 | 1282 | ATTGTTAGAAAAGTGTAGATTAAAG |
| 111 | 1283 | ATGAGTATGTTATTAGTGTATGTA |
| 112 | 1284 | TGTAATAGTGAAGTTAGATTGTAT |
| 113 | 1285 | ATTGATAGATGATTAGTTAGTTGA |
| 114 | 1286 | ATGAGTTTGTATTATGAGATTAAAG |
| 115 | 1287 | TGATGTTTGATTATGATGTAGTAT |
| 116 | 1288 | ATGAGTTAGTTATGAATTAGATGA |
| 117 | 1289 | ATTGTTAGTGATGTTAGTAATTAG |
| 118 | 1290 | TGATGTAAGTATTGATGTTAGTTT |
| 119 | 1291 | GATTGTAAATAGAAAAGTGAAGTAA |
| 120 | 1292 | ATTGTGTATGAAGTATTGTATGAT |
| 121 | 1293 | ATAGTGATGTTATGAAGATTGTTA |
| 122 | 1294 | TTAGATGAATTGTGAAGTATTTAG |
| 123 | 1295 | GTAAGTTATGATTGATGTTATGAA |
| 124 | 1296 | GTATTGATGTTTAAAGTGTAAATAG |
| 125 | 1297 | GATTGTAAAGTAAGATTGTATATTG |
| 126 | 1298 | GTTTGTATTTAGATGAATAGAAAAG |
| 127 | 1299 | GTTTGATTTGTAATAGTGATTGTA |
| 128 | 1300 | TGTATGTAGTATTTAGAAAAGATGA |

| SEQ ID NO(1) | Sequence | No Assigned in Example 3 | |
|----------------|-----------------|--------------------------------------|-----|
| 129 | 1301 | ATGAATTGTGATAAAGAAAAGTTAG | |
| 130 | 1302 | TTAGTGTAGTAAGTTTAAAGTGTA | 95 |
| 131 | 1303 | GTATGATTGTTTGTAAATTAGTGAT | |
| 132 | 1304 | GTTTAAAGTTAGTTGAGTTAGTAT | 96 |
| 133 | 1305 | ATAGTGTATGTAGATTATGAGATT | 97 |
| 134 | 1306 | TTGAATGATTAGTTGAGTATGATT | 98 |
| 135 | 1307 | GTATGTAAGTTAGTATGATTTGAA | |
| 136 | 1308 | TGTAGTATATTGTTGAATTGTGAT | |
| 137 | 1309 | ATAGTGATTGTATGTATGATAAAG | |
| 138 | 1310 | TTAGTGATTGATGTATATTGAAAG | |
| 139 | 1311 | GTAAGATTATGAGTTATGATGTAA | |
| 140 | 1312 | GTTATGAAATTGTTAGTGTAGATT | 99 |
| 141 | 1313 | GTTAGATTTGTAGTTTAAAGATAG | 100 |
| 142 | 1314 | TTAGTGATTGAAATGATGTAGATT | |
| 143 | 1315 | AAAGTGTAGTTATTAGTTAGTTAG | |
| 144 | 1316 | AAAGAAAGTGTATGATGTTATTAG | |
| 145 | 1317 | GATTGTATATTGTGTATGATGATT | |
| 146 | 1318 | TTGAGATTGTTATGATATGAGTAT | |
| 147 | 1319 | ATGAGTATGATTGTTATGATGTTT | |
| 148 | 1320 | TGATTTAGTGAAATTGTGTATTAG | |
| 149 | 1321 | TGAATGTATGTAGTATGTTTGTTA | |
| 150 | 1322 | GTTAGTATTGATGATTATGAGTTA | |
| 151 | 1323 | GTATATTGTGATTTAGTTGAGATT | |
| 152 | 1324 | GTTAGTTTAAAGTTGAGATTGTTT | |
| 153 | 1325 | GTATATTGTTAGATGAGATTTGTA | |
| 154 | 1326 | TGATGTATGTTAGTTTATGAATGA | |
| 155 | 1327 | TGTAGTATGTAATGTAGTATTTGA | |
| 156 | 1328 | ATGAGTTATGTATTGAGTTAGTAT | |
| 157 | 1329 | TGTATGATGATTATAGTTGAGTAA | |
| 158 | 1330 | ATTGATGAATGAGTTTGTATAAAG | |
| 159 | 1331 | TTGAGTTTATGATTAGAAAGAAAG | |
| 160 | 1332 | TGATATTGATGAGTTAGTATTGAA | |
| 161 | 1333 | ATAGAAAGTGAAATGAGTATGTTA | |
| 162 | 1334 | TTGATGTAGATTTGATGTATATAG | |
| 163 | 1335 | TTGAGATTATAGTGTAGTTTATAG | |
| 164 | 1336 | TGATGTTAGATTGTTTGATTATTG | |
| 165 | 1337 | TGTATTAGATAGTGATTTGAATGA | |
| 166 | 1338 | GATTATGATGAATGTAGTATGTAA | |
| 167 | 1339 | TGAATGATTGATATGAATAGTGTA | |
| 168 | 1340 | GTAATGATTTAGTGTATTGAGTTT | |
| 169 | 1341 | TGTAGTAATGATTTGATGATAAAG | |
| 170 | 1342 | TGAAGATTGTTATTAGTGATATTG | |
| 171 | 1343 | GTATTTGAATGATGTAATAGTGTA | |
| 172 | 1344 | GTATATGATGTATTAGATTGAAAG | |
| 173 | 1345 | AAAGTTAGATTGAAAGTGATAAAG | |
| 174 | 1346 | GTAAGATGTTGATATAGAAGATTA | 9 |
| 175 | 1347 | TAATATGAGATGAAAGTGAATTAG | |
| 176 | 1348 | TTAGTGAAGAAGTATAGTTTATTG | 13 |
| 177 | 1349 | GTAGTTGAGAAGATAGTAATTAAT | |
| 178 | 1350 | ATGAGATGATATTTGAGAAGTAAT | |
| 179 | 1351 | GATGTGAAGAAGATGAATATATAT | |
| 180 | 1352 | AAAGTATAGTAAGATGTATAGTAG | 14 |
| 181 | 1353 | GAAGTAATATGAGTAGTTGAATAT | |

| SEQ ID NO (1) | Sequence | No Assigned in Example 3 |
|---------------------|----------------------------|--------------------------|
| 182 1354 | TTGATAATGTTTGTGTTGTGTTGTAG | 28 |
| 183 1355 | TGAAGAAGAAAGTATAATGATGAA | |
| 184 1356 | GTAGATTAGTTTGAAGTGAATAAT | 32 |
| 185 1357 | TATAGTAGTGAAGATGATATATGA | |
| 186 1358 | TATAATGAGTTGTTAGATATGTTG | |
| 187 1359 | GTTGTGAAATTAGATGTGAAATAT | |
| 188 1360 | TAATGTTGTGAATAATGTAGAAAG | 40 |
| 189 1361 | GTTTATAGTGAAATATGAAGATAG | 42 |
| 190 1362 | ATTATGAAGTAAGTTAATGAGAAG | 47 |
| 191 1363 | GATGAAAGTAATGTTTATTGTGAA | |
| 192 1364 | ATTATTGAGATGTGAAGTTTGT | 48 |
| 193 1365 | TGTAGAAGATGAGATGTATAATTA | 53 |
| 194 1366 | TAATTTGAGTTGTGTATATAGTAG | |
| 195 1367 | TGATATTAGTAAGAAGTTGAATAG | |
| 196 1368 | GTTAGTTATTGAGAAGTGTATATA | 55 |
| 197 1369 | GTAGTAATGTTAATGAATTAGTAG | 58 |
| 198 1370 | GTTTGTGTTGATGTGATTGAATAAT | |
| 199 1371 | GTAAGTAGTAATTTGAATATGTAG | 64 |
| 200 1372 | GTTTGAAGATATGTTTGAAGTATA | |
| 201 1373 | ATGATAATTGAAGATGTAATGTTG | |
| 202 1374 | GTAGATAGTATAGTTGTAATGT | 66 |
| 203 1375 | GATGTGAATGTAATATGTTTATAG | 69 |
| 204 1376 | TGAAATTAGTTTGTAAGATGTGTA | 74 |
| 205 1377 | TGTAGTATAAAGTATATGAAGTAG | 63 |
| 206 1378 | ATATGTTGTTGAGTTGATAGTATA | 89 |
| 207 1379 | ATTATTGAGTAGAAAGATAGAAAG | 94 |
| 208 1380 | GTTGTTGAATATTGAATATAGTTG | |
| 209 1381 | ATGAGAAGTTAGTAATGTAAATAG | |
| 210 1382 | TGAAATGAGAAGATTAATGAGTTT | |

Please insert the sequence listing provided on pages 1/368 to 368/368 in the accompanying Response to the Notice to File Missing Parts of June 21, 2004, and submitted under separate cover, into the disclosure.